

GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on: August 21, 2006, 23:30:26 ; Search time 196 Seconds

(without alignments)  
11.664 Million cell updates/sec

Title: US-10-766-527-1

Perfect score: 31

Sequence: 1 YGFGG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 300 summaries

## Database :

A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1980s:\*

3: geneseqp2000s:\*

4: geneseqp2000s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	5	2	AAR76124 Osteogeni
2	31	100.0	5	2	ADC73232 Cycliic ps
3	31	100.0	5	6	ABP72525 Osteogeni
4	31	100.0	6	2	AAR62388 Osteoblas
5	31	100.0	6	2	AAR62954 Osteogeni
6	31	100.0	6	2	ADC73230 Cycliic ps
7	31	100.0	6	2	ADC73233 Cycliic ps
8	31	100.0	6	2	ADC73229 Cycliic ps
9	31	100.0	6	6	ABP72528 Osteogeni
10	31	100.0	6	8	ADV78752 Hemoprot
11	31	100.0	14	2	AAR06551 Osteogeni
12	31	100.0	14	2	AAR43890 Osteogeni
13	31	100.0	14	2	AAR43888 Osteogeni
14	31	100.0	14	2	AAR62952 Osteogeni
15	31	100.0	14	4	AAB92061 Growth fa
16	31	100.0	14	6	ABR63887 Osteogeni
17	31	100.0	14	6	ADA27392 Osteogeni
18	31	100.0	14	8	ADA35204 Human OGP
19	31	100.0	14	9	AEC78137 Osteogeni
20	31	100.0	14	9	AED35403 Drug deli
21	31	100.0	14	9	AED61987 Osteogeni
22	31	100.0	15	2	AAR43889 Osteogeni
23	31	100.0	17	2	AAR48440 Histogran

24	31	100.0	17	2	AAR48449 Histogran
25	31	100.0	17	2	AAR48442 Histogran
26	31	100.0	17	2	AAR48448 Histogran
27	31	100.0	17	2	AAR48444 Histogran
28	31	100.0	17	2	AAR48445 Histogran
29	31	100.0	17	2	AAR48450 Histogran
30	31	100.0	17	2	AAR48443 Histogran
31	31	100.0	17	2	AAR48447 Histogran
32	31	100.0	17	2	AAR48446 Histogran
33	31	100.0	17	2	AAR48441 Histogran
34	31	100.0	17	9	AED35422 Drug deli
35	31	100.0	17	9	AED35421 Drug deli
36	31	100.0	20	9	AED35418 Drug deli
37	31	100.0	20	9	AED35419 Drug deli
38	31	100.0	20	9	AED35420 Drug deli
39	31	100.0	21	9	AED61989 Osteogeni
40	31	100.0	25	9	AED61991 Osteogeni
41	31	100.0	90	4	AM17849 Peptide #
42	31	100.0	90	4	AB36867 Peptide #
43	31	100.0	90	4	AM30355 Peptide #
44	31	100.0	90	4	AB31654 Peptide #
45	31	100.0	90	4	AB322193 Protein #
46	31	100.0	90	4	AM570017 Human bon
47	31	100.0	90	4	AM57613 Human bra
48	31	100.0	90	4	AB31713 Human liv
49	31	100.0	90	4	AM05496 Peptide #
50	31	100.0	90	5	AB39647 Human pep
51	31	100.0	91	9	ADM17338 Eucalyptu
52	31	100.0	93	9	ADM17339 Eucalyptu
53	31	100.0	102	2	AY07283 Human his
54	31	100.0	102	2	AY07282 Histone H
55	31	100.0	102	2	AY05481 Human his
56	31	100.0	102	2	AY05480 Consensus
57	31	100.0	102	7	ADD45890 Rat Proce
58	31	100.0	102	7	ADB60487 Human pro
59	31	100.0	102	7	ADD45892 Human pro
60	31	100.0	102	7	ADB60485 Rat Proce
61	31	100.0	102	7	ADF89426 Human his
62	31	100.0	102	7	ADF68267 Human hea
63	31	100.0	102	8	ADF71922 Yeast wll
64	31	100.0	102	8	ADF71923 Yeast his
65	31	100.0	102	8	ADF71925 Yeast his
66	31	100.0	102	8	ADF48808 Human his
67	31	100.0	102	8	ADT58370 Plant pol
68	31	100.0	102	9	AED66775 S. cerevi
69	31	100.0	103	3	AG40967 Zea maye
70	31	100.0	103	3	AG40967 Zea maye
71	31	100.0	103	3	AG40967 Zea maye
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78	31	100.0	103	3	AG40967 Zea maye
79	31	100.0	103	3	AG40967 Zea maye
80	31	100.0	103	3	AG40967 Zea maye
81	31	100.0	103	3	AG40967 Zea maye
82	31	100.0	103	3	AG40967 Zea maye
83	31	100.0	103	3	AG40967 Zea maye
84	31	100.0	103	3	AG40967 Zea maye
85	31	100.0	103	3	AG40967 Zea maye
86	31	100.0	103	3	AG40967 Zea maye
87	31	100.0	103	3	AG40967 Zea maye
88	31	100.0	103	3	AG40967 Zea maye
89	31	100.0	103	3	AG40967 Zea maye
90	31	100.0	103	3	AG40967 Zea maye
91	31	100.0	103	3	AG40967 Zea maye
92	31	100.0	103	3	AG40967 Zea maye
93	31	100.0	103	3	AG40967 Zea maye
94	31	100.0	103	3	AG40967 Zea maye
95	31	100.0	103	3	AG40967 Zea maye
96	31	100.0	103	3	AG40967 Zea maye

STC sequence search results

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OM protein - protein search, using sw model

Run on: August 21, 2006, 23:39:22 ; Search time 52 Seconds  
(without alignments)  
8.416 Million cell updates/sec

Title: US-10-766-527-1  
Perfect score: 31  
Sequence: 1 YGFG 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues  
Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Issued Patents, AA.\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/5.COMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/6.COMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/7.COMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/H.COMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/PCPUS.COMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/RE.COMB.pep.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	31	100.0	5	1	US-08-530-277-1
2	31	100.0	5	2	US-09-150-621-4
3	31	100.0	5	2	US-09-150-621-6
4	31	100.0	5	2	US-09-150-621-7
5	31	100.0	5	2	US-09-150-621-8
6	31	100.0	5	2	US-09-150-621-9
7	31	100.0	5	2	US-09-150-621-10
8	31	100.0	5	2	US-09-150-621-27
9	31	100.0	5	2	US-09-150-621-32
10	31	100.0	5	2	US-09-150-621-35
11	31	100.0	5	2	US-09-150-621-47
12	31	100.0	5	2	US-09-150-621-48
13	31	100.0	5	2	US-09-150-621-49
14	31	100.0	5	2	US-09-150-621-50
15	31	100.0	5	2	US-09-150-621-51
16	31	100.0	5	2	US-09-150-621-61
17	31	100.0	6	1	US-08-530-277-6
18	31	100.0	6	2	US-09-150-621-38
19	31	100.0	6	2	US-09-150-621-39
20	31	100.0	6	2	US-09-150-621-40
21	31	100.0	6	2	US-09-150-621-41
22	31	100.0	6	2	US-09-150-621-53
23	31	100.0	6	2	US-09-150-621-59
24	31	100.0	10	7	5461034-5
25	31	100.0	11	7	5461034-4
26	31	100.0	12	7	5461034-3

27	31	100.0	13	7	5461034-2	Patent No. 5461034
28	31	100.0	14	1	US-08-530-277-4	Sequence 1, Appl
29	31	100.0	14	2	US-09-150-621-1	Sequence 12, Appl
30	31	100.0	14	2	US-09-150-621-54	Sequence 54, Appl
31	31	100.0	14	2	US-09-150-621-55	Sequence 55, Appl
32	31	100.0	14	2	US-09-623-548A-1237	Sequence 1237, Ap
33	31	100.0	14	2	US-09-657-276-1237	Sequence 1237, Ap
34	31	100.0	14	2	US-10-066-905-3	Sequence 3, Appl
35	31	100.0	15	7	5461034-1	Patent No. 5461034
36	31	100.0	15	2	US-09-530-123B-13	Sequence 13, Appl
37	31	100.0	15	2	US-10-437-435-13	Sequence 13, Appl
38	31	100.0	103	2	US-09-949-016-6380	Sequence 6380, Ap
39	31	100.0	103	2	US-09-949-016-6381	Sequence 6381, Ap
40	31	100.0	103	2	US-09-949-016-6382	Sequence 6382, Ap
41	31	100.0	103	2	US-09-949-016-6388	Sequence 6388, Ap
42	31	100.0	107	2	US-09-248-796A-18645	Sequence 18645, A
43	31	100.0	111	2	US-09-949-016-8136	Sequence 8136, Ap
44	31	100.0	115	2	US-09-248-796A-18646	Sequence 18646, A
45	31	100.0	120	2	US-09-949-016-8186	Sequence 8186, Ap
46	31	100.0	122	2	US-09-949-016-8187	Sequence 8187, Ap
47	31	100.0	141	2	US-09-949-016-8229	Sequence 8229, Ap
48	31	100.0	151	2	US-09-270-767-45274	Sequence 45274, A
49	31	100.0	213	2	US-09-252-991A-29929	Sequence 29929, A
50	31	100.0	220	2	US-09-902-540-12909	Sequence 12909, A
51	31	100.0	272	2	US-09-248-796A-21180	Sequence 21180, A
52	31	100.0	290	2	US-09-602-787A-670	Sequence 670, App
53	31	100.0	319	2	US-09-134-001C-3888	Sequence 3888, Ap
54	31	100.0	344	2	US-08-311-721A-82	Sequence 82, Appl
55	31	100.0	370	2	US-09-342-143-2	Sequence 2, Appl
56	31	100.0	370	2	US-09-924-439-2	Sequence 2935, Ap
57	31	100.0	372	2	US-09-540-047-2935	Sequence 16, Appl
58	31	100.0	417	2	US-09-710-262E-16	Sequence 2752, Ap
59	31	100.0	419	2	US-09-583-110-2752	Sequence 3716, Ap
60	31	100.0	425	2	US-09-107-433-3776	Sequence 15197, A
61	31	100.0	428	2	US-09-248-796A-15197	Sequence 2, Appl
62	31	100.0	465	2	US-08-788-231A-2	Sequence 2, Appl
63	31	100.0	465	2	US-09-495-229A-2	Sequence 4, Appl
64	31	100.0	465	2	US-09-043-944-4	Sequence 4, Appl
65	31	100.0	465	2	US-10-811-199-4	Sequence 1, Appl
66	31	100.0	546	1	US-09-067-351-1	Sequence 1, Appl
67	31	100.0	546	2	US-09-360-490-1	Sequence 6628, Ap
68	31	100.0	564	2	US-09-949-016-6628	Sequence 3772, Ap
69	31	100.0	567	2	US-10-104-047-3772	Sequence 11035, A
70	31	100.0	569	2	US-09-949-016-11035	Sequence 11036, A
71	31	100.0	569	2	US-09-949-016-11036	Sequence 4334, A
72	31	100.0	599	2	US-09-107-433-4334	Sequence 2449, Ap
73	31	100.0	967	2	US-09-540-236-2449	Sequence 6, Appl
74	31	100.0	974	2	US-08-960-048-6	Sequence 3366, Ap
75	31	100.0	974	2	US-09-838-586-6	Sequence 12, Appl
76	31	100.0	1032	1	US-09-583-110-3366	Sequence 28, Appl
77	31	100.0	1876	1	US-08-609-049A-12	Sequence 28, Appl
78	31	100.0	1876	2	US-08-609-049A-28	Sequence 28, Appl
79	31	100.0	1876	2	US-09-170-996-12	Sequence 28, Appl
80	31	100.0	1876	2	US-09-170-996-28	Sequence 4, Appl
81	31	100.0	24	2	US-09-142-732-4	Sequence 6070, Ap
82	31	100.0	110	2	US-09-513-999C-6070	Sequence 3, Appl
83	31	100.0	125	2	US-09-199-149-3	Sequence 43889, A
84	31	100.0	150	2	US-09-270-767-43889	Sequence 4741, Ap
85	31	100.0	203	2	US-09-543-661A-4741	Sequence 14367, A
86	31	100.0	251	2	US-09-489-039A-14267	Sequence 455, App
87	31	100.0	263	2	US-09-303-518D-452	Sequence 26, Appl
88	31	100.0	350	2	US-09-913-064A-26	Sequence 19913, A
89	31	100.0	392	2	US-09-248-796A-19913	Sequence 124, App
90	31	100.0	395	2	US-09-270-767-43336	Sequence 125, App
91	31	100.0	407	2	US-09-949-016-7916	Sequence 146, App
92	31	100.0	438	2	US-09-044-718-2	Sequence 147, App
93	31	100.0	438	2	US-10-062-848-2	Sequence 2, Appl
94	31	100.0	440	2	US-09-684-855-101	Sequence 101, App
95	31	100.0	440	2	US-09-684-855-102	Sequence 102, App
96	31	100.0	440	2	US-09-684-855-124	Sequence 124, App
97	31	100.0	440	2	US-09-684-855-125	Sequence 146, App
98	31	100.0	440	2	US-09-684-855-146	Sequence 147, App
99	31	100.0	440	2	US-09-684-855-147	Sequence 147, App

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OM protein - protein search, using sw model

Run on: August 21, 2006, 23:40:01 ; Search time 183 Seconds  
(without alignments)  
12.656 Million cell updates/sec

Title: US-10-766-527-1  
Perfect score: 31  
Sequence: 1 YFGG 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA Main:

1: /EMC\_Celextra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celextra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celextra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celextra\_SIDS3/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
5: /EMC\_Celextra\_SIDS3/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
6: /EMC\_Celextra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	5	US-10-255-679-4	Sequence 4, Appli
2	31	100.0	5	US-10-255-679-6	Sequence 6, Appli
3	31	100.0	5	US-10-255-679-7	Sequence 7, Appli
4	31	100.0	5	US-10-255-679-8	Sequence 8, Appli
5	31	100.0	5	US-10-255-679-9	Sequence 9, Appli
6	31	100.0	5	US-10-255-679-10	Sequence 10, Appli
7	31	100.0	5	US-10-255-679-27	Sequence 27, Appli
8	31	100.0	5	US-10-255-679-32	Sequence 32, Appli
9	31	100.0	5	US-10-255-679-35	Sequence 35, Appli
10	31	100.0	5	US-10-255-679-47	Sequence 47, Appli
11	31	100.0	5	US-10-255-679-48	Sequence 48, Appli
12	31	100.0	5	US-10-255-679-49	Sequence 49, Appli
13	31	100.0	5	US-10-255-679-50	Sequence 50, Appli
14	31	100.0	5	US-10-255-679-51	Sequence 51, Appli
15	31	100.0	5	US-10-255-679-61	Sequence 61, Appli
16	31	100.0	5	US-10-766-527-1	Sequence 1, Appli
17	31	100.0	6	US-10-255-679-38	Sequence 38, Appli
18	31	100.0	6	US-10-255-679-39	Sequence 39, Appli
19	31	100.0	6	US-10-255-679-40	Sequence 40, Appli
20	31	100.0	6	US-10-255-679-41	Sequence 41, Appli
21	31	100.0	6	US-10-255-679-53	Sequence 53, Appli
22	31	100.0	6	US-10-255-679-59	Sequence 59, Appli
23	31	100.0	6	US-10-766-527-4	Sequence 4, Appli
24	31	100.0	14	US-10-255-679-1	Sequence 54, Appli
25	31	100.0	14	US-10-255-679-54	Sequence 55, Appli
26	31	100.0	14	US-10-255-679-55	Sequence 56, Appli
27	31	100.0	14	US-10-068-905-3	Sequence 3, Appli

28	31	100.0	14	US-11-066-697-1237	Sequence 1237, Ap
29	31	100.0	14	US-11-079-632-3	Sequence 3, Appli
30	31	100.0	15	US-10-437-435-13	Sequence 13, Appli
31	31	100.0	47	US-10-425-115-208585	Sequence 208585,
32	31	100.0	61	US-10-425-115-276451	Sequence 276451,
33	31	100.0	62	US-10-425-115-194986	Sequence 194986,
34	31	100.0	62	US-10-425-115-340102	Sequence 340102,
35	31	100.0	63	US-10-425-115-263659	Sequence 263659,
36	31	100.0	63	US-10-425-115-300116	Sequence 300116,
37	31	100.0	63	US-10-425-115-340091	Sequence 340091,
38	31	100.0	63	US-10-425-115-290982	Sequence 290982,
39	31	100.0	73	US-10-425-115-259714	Sequence 259714,
40	31	100.0	79	US-10-425-115-312112	Sequence 312112,
41	31	100.0	82	US-10-425-115-190140	Sequence 190140,
42	31	100.0	83	US-10-425-115-259653	Sequence 259653,
43	31	100.0	84	US-10-424-599-162967	Sequence 162967,
44	31	100.0	90	US-09-864-761-37491	Sequence 37491, A
45	31	100.0	92	US-10-767-701-59845	Sequence 59845, A
46	31	100.0	93	US-10-424-599-159204	Sequence 159204,
47	31	100.0	99	US-10-425-115-259631	Sequence 259631,
48	31	100.0	102	US-10-408-765A-73	Sequence 73, Appli
49	31	100.0	102	US-10-739-930-8447	Sequence 8447, Ap
50	31	100.0	102	US-10-425-115-301864	Sequence 301864,
51	31	100.0	103	US-10-108-605-81	Sequence 81, Appli
52	31	100.0	103	US-10-108-605-159	Sequence 159, App
53	31	100.0	103	US-10-291-307-21	Sequence 21, Appli
54	31	100.0	103	US-10-451-467A-38	Sequence 38, Appli
55	31	100.0	103	US-10-451-467A-324	Sequence 324, App
56	31	100.0	103	US-10-451-467A-682	Sequence 682, App
57	31	100.0	103	US-10-477-369-21	Sequence 21, Appli
58	31	100.0	103	US-10-767-701-47214	Sequence 47214, A
59	31	100.0	103	US-10-767-701-47215	Sequence 47215, A
60	31	100.0	103	US-10-425-115-323722	Sequence 323722,
61	31	100.0	103	US-10-739-930-5693	Sequence 5693, Ap
62	31	100.0	103	US-10-739-930-10425	Sequence 10425, A
63	31	100.0	103	US-10-756-149-4800	Sequence 4800, Ap
64	31	100.0	103	US-10-631-467-731	Sequence 731, App
65	31	100.0	103	US-11-097-143-6348	Sequence 6348, Ap
66	31	100.0	103	US-11-116-959-2	Sequence 2, Appli
67	31	100.0	105	US-10-424-599-145124	Sequence 145124,
68	31	100.0	105	US-10-451-467A-592	Sequence 592, App
69	31	100.0	105	US-10-451-467A-626	Sequence 626, App
70	31	100.0	107	US-10-425-115-340094	Sequence 340094,
71	31	100.0	109	US-10-425-115-191448	Sequence 191448,
72	31	100.0	111	US-10-767-701-54484	Sequence 54484, A
73	31	100.0	111	US-10-739-930-10567	Sequence 10567, A
74	31	100.0	111	US-10-450-763-54484	Sequence 54484, A
75	31	100.0	113	US-10-437-963-132567	Sequence 132567,
76	31	100.0	113	US-10-437-963-181832	Sequence 181832,
77	31	100.0	115	US-10-425-115-272964	Sequence 272964, A
78	31	100.0	119	US-10-767-701-47208	Sequence 47208, A
79	31	100.0	120	US-09-925-300-1294	Sequence 1294, Ap
80	31	100.0	121	US-10-425-115-213180	Sequence 213180,
81	31	100.0	123	US-10-739-930-10138	Sequence 10138, A
82	31	100.0	128	US-10-767-701-47217	Sequence 47217, A
83	31	100.0	130	US-10-767-701-47210	Sequence 47210, A
84	31	100.0	132	US-10-424-599-250207	Sequence 250207,
85	31	100.0	133	US-10-029-386-11454	Sequence 31454, A
86	31	100.0	133	US-10-767-701-47213	Sequence 47213, A
87	31	100.0	135	US-10-767-701-47209	Sequence 47209, A
88	31	100.0	137	US-10-424-599-335505	Sequence 235505,
89	31	100.0	139	US-10-767-701-47212	Sequence 47212, A
90	31	100.0	139	US-10-425-115-117346	Sequence 317346,
91	31	100.0	140	US-10-767-701-47211	Sequence 47211, A
92	31	100.0	151	US-10-437-963-190692	Sequence 190692,
93	31	100.0	152	US-10-479-435-5	Sequence 5, Appli
94	31	100.0	159	US-10-424-599-146318	Sequence 146318,
95	31	100.0	159	US-11-087-099-2681	Sequence 2681, Ap
96	31	100.0	165	US-11-079-463-7361	Sequence 7361, Ap
97	31	100.0	165	US-11-079-463-8718	Sequence 8718, Ap
98	31	100.0	181	US-10-425-115-280932	Sequence 280932,
99	31	100.0	185	US-09-988-067B-56	Sequence 56, Appli
100	31	100.0	189	US-11-079-463-7884	Sequence 7884, Ap

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OM protein - protein search, using sw model

Run on: August 21, 2006, 23:40:56 ; Search time 32 Seconds

(without alignments)  
10.587 Million cell updates/sec

Title: US-10-766-527-1

Perfect score: 31

Sequence: 1 YGFGG 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 243793 segs, 67754213 residues

Total number of hits satisfying chosen parameters: 243793

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications AA New:\*  
1: /EMC\_Celettera\_SIDS3/ptodata/2/pubppaa/US09\_NEW\_PUB pep:\*  
2: /EMC\_Celettera\_SIDS3/ptodata/2/pubppaa/US06\_NEW\_PUB pep:\*  
3: /EMC\_Celettera\_SIDS3/ptodata/2/pubppaa/US07\_NEW\_PUB pep:\*  
4: /EMC\_Celettera\_SIDS3/ptodata/2/pubppaa/US08\_NEW\_PUB pep:\*  
5: /EMC\_Celettera\_SIDS3/ptodata/2/pubppaa/US10\_NEW\_PUB pep:\*  
6: /EMC\_Celettera\_SIDS3/ptodata/2/pubppaa/US11\_NEW\_PUB pep:\*  
7: /EMC\_Celettera\_SIDS3/ptodata/2/pubppaa/US11\_NEW\_PUB pep:\*  
8: /EMC\_Celettera\_SIDS3/ptodata/2/pubppaa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	102	7	US-11-056-355B-11191
2	31	100.0	103	6	US-10-953-349-71
3	31	100.0	103	6	US-10-953-349-2421
4	31	100.0	103	6	US-10-953-349-10509
5	31	100.0	103	6	US-10-953-349-14785
6	31	100.0	103	6	US-10-953-349-15070
7	31	100.0	103	6	US-10-953-349-15185
8	31	100.0	103	6	US-10-953-349-15200
9	31	100.0	103	6	US-10-953-349-15303
10	31	100.0	103	6	US-10-953-349-15371
11	31	100.0	103	6	US-10-953-349-16224
12	31	100.0	103	6	US-10-953-349-18365
13	31	100.0	103	6	US-10-953-349-20454
14	31	100.0	103	6	US-10-953-349-28310
15	31	100.0	103	6	US-10-953-349-28545
16	31	100.0	103	6	US-10-953-349-30050
17	31	100.0	103	6	US-10-953-349-30857
18	31	100.0	103	6	US-10-953-349-35714
19	31	100.0	103	6	US-10-953-349-38640
20	31	100.0	103	6	US-10-953-349-38840
21	31	100.0	103	6	US-10-449-902-29037
22	31	100.0	103	6	US-10-449-902-29097
23	31	100.0	103	6	US-10-449-902-29410
24	31	100.0	103	6	US-10-449-902-29494
25	31	100.0	103	6	US-10-449-902-36925

26	31	100.0	103	7	US-11-105-223-40	Sequence 40, App1
27	31	100.0	103	7	US-11-056-355B-7737	Sequence 7737, App
28	31	100.0	103	7	US-11-056-355B-10506	Sequence 10506, A
29	31	100.0	103	7	US-11-056-355B-14810	Sequence 14810, A
30	31	100.0	103	7	US-11-056-355B-15141	Sequence 15141, A
31	31	100.0	103	7	US-11-056-355B-15174	Sequence 15174, A
32	31	100.0	103	7	US-11-056-355B-20933	Sequence 20933, A
33	31	100.0	103	7	US-11-056-355B-21693	Sequence 21693, A
34	31	100.0	103	7	US-11-056-355B-22100	Sequence 22100, A
35	31	100.0	103	7	US-11-056-355B-26986	Sequence 26986, A
36	31	100.0	103	7	US-11-056-355B-29262	Sequence 29262, A
37	31	100.0	103	7	US-11-056-355B-29882	Sequence 29882, A
38	31	100.0	103	7	US-11-056-355B-32856	Sequence 32856, A
39	31	100.0	103	7	US-11-056-355B-33392	Sequence 33392, A
40	31	100.0	103	7	US-11-056-355B-35251	Sequence 35251, A
41	31	100.0	103	7	US-11-056-355B-36429	Sequence 36429, A
42	31	100.0	103	7	US-11-056-355B-72009	Sequence 72009, A
43	31	100.0	103	7	US-11-056-355B-72011	Sequence 72011, A
44	31	100.0	103	7	US-11-056-355B-73525	Sequence 73525, A
45	31	100.0	103	7	US-11-056-355B-74607	Sequence 74607, A
46	31	100.0	103	7	US-11-056-355B-84705	Sequence 84705, A
47	31	100.0	103	7	US-11-056-355B-101142	Sequence 101142, A
48	31	100.0	103	7	US-11-056-355B-112381	Sequence 112381, A
49	31	100.0	108	6	US-10-953-349-15184	Sequence 15184, A
50	31	100.0	109	6	US-10-953-349-70	Sequence 70, App1
51	31	100.0	111	7	US-11-056-355B-20534	Sequence 20534, A
52	31	100.0	111	7	US-11-056-355B-72510	Sequence 72510, A
53	31	100.0	113	6	US-10-449-902-38864	Sequence 38864, A
54	31	100.0	116	7	US-11-056-355B-22099	Sequence 22099, A
55	31	100.0	123	7	US-11-056-355B-15140	Sequence 15140, A
56	31	100.0	124	6	US-10-953-349-10508	Sequence 10508, A
57	31	100.0	124	6	US-11-056-355B-21692	Sequence 21692, A
58	31	100.0	125	6	US-10-953-349-15199	Sequence 15199, A
59	31	100.0	127	6	US-10-953-349-14784	Sequence 14784, A
60	31	100.0	127	6	US-10-953-349-15302	Sequence 15302, A
61	31	100.0	127	6	US-10-953-349-20453	Sequence 20453, A
62	31	100.0	127	6	US-10-953-349-28544	Sequence 28544, A
63	31	100.0	128	7	US-11-056-355B-15313	Sequence 15313, A
64	31	100.0	129	6	US-10-953-349-16223	Sequence 16223, A
65	31	100.0	129	6	US-10-953-349-10856	Sequence 10856, A
66	31	100.0	129	6	US-10-953-349-15713	Sequence 15713, A
67	31	100.0	129	6	US-10-953-349-38839	Sequence 38839, A
68	31	100.0	129	7	US-11-056-355B-7736	Sequence 7736, App
69	31	100.0	129	7	US-11-056-355B-14809	Sequence 14809, A
70	31	100.0	133	7	US-11-056-355B-10505	Sequence 10505, A
71	31	100.0	134	6	US-10-953-349-15069	Sequence 15069, A
72	31	100.0	134	7	US-11-056-355B-11190	Sequence 11190, A
73	31	100.0	134	6	US-10-953-349-28309	Sequence 28309, A
74	31	100.0	134	6	US-10-449-902-54526	Sequence 54526, A
75	31	100.0	214	6	US-10-449-902-55835	Sequence 55835, A
76	31	100.0	214	6	US-10-542-508-48	Sequence 48, App1
77	31	100.0	235	6	US-10-953-349-35009	Sequence 35009, A
78	31	100.0	235	7	US-11-056-355B-35702	Sequence 35702, App
79	31	100.0	235	7	US-11-056-355B-12224	Sequence 12224, App
80	31	100.0	238	6	US-10-953-349-35008	Sequence 35008, A
81	31	100.0	238	7	US-11-056-355B-3571	Sequence 3571, App
82	31	100.0	238	7	US-11-056-355B-12223	Sequence 12223, A
83	31	100.0	248	6	US-10-953-349-28521	Sequence 28521, A
84	31	100.0	248	7	US-11-056-355B-65409	Sequence 65409, A
85	31	100.0	254	7	US-11-056-355B-35707	Sequence 35707, A
86	31	100.0	254	7	US-11-056-355B-3570	Sequence 3570, App
87	31	100.0	254	7	US-11-056-355B-12222	Sequence 12222, A
88	31	100.0	307	6	US-10-953-349-28540	Sequence 28540, A
89	31	100.0	307	7	US-11-056-355B-65408	Sequence 65408, A
90	31	100.0	308	7	US-11-056-355B-23802	Sequence 23802, A
91	31	100.0	316	6	US-10-471-571A-242	Sequence 242, App
92	31	100.0	317	6	US-10-449-902-77457	Sequence 77457, A
93	31	100.0	322	6	US-10-449-902-29886	Sequence 29886, A
94	31	100.0	334	7	US-11-330-403-8303	Sequence 8303, App
95	31	100.0	338	6	US-10-449-902-11860	Sequence 11860, A
96	31	100.0	343	7	US-11-330-403-16606	Sequence 16606, A
97	31	100.0	346	7	US-11-330-403-9877	Sequence 9877, App
98	31	100.0	347	7	US-11-330-403-18140	Sequence 18140, A

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OM protein - protein search, using sw model

Run on: August 21, 2006, 23:34:21 / Search time 38 Seconds  
(without alignments)  
12.660 Million cell updates/sec

Title: US-10-766-527-1

Perfect score: 31

Sequence: 1 YGFGS 5

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database:

PIR\_80:\*  
1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	14	2	151432
2	31	100.0	18	2	C30309
3	31	100.0	32	2	S13897
4	31	100.0	45	2	C21440
5	31	100.0	55	2	I48404
6	31	100.0	85	2	S00071
7	31	100.0	101	2	JS0314
8	31	100.0	102	1	HSTR4
9	31	100.0	102	1	HSTR4
10	31	100.0	102	1	HSTR4
11	31	100.0	102	1	HSTR4
12	31	100.0	102	1	HSTR4
13	31	100.0	102	1	HSTR4
14	31	100.0	102	1	HSTR4
15	31	100.0	102	1	HSTR4
16	31	100.0	102	1	HSTR4
17	31	100.0	102	1	HSTR4
18	31	100.0	103	1	HSTR4
19	31	100.0	103	1	HSTR4
20	31	100.0	103	1	HSTR4
21	31	100.0	103	1	HSTR4
22	31	100.0	103	1	HSTR4
23	31	100.0	103	1	HSTR4
24	31	100.0	103	1	HSTR4
25	31	100.0	103	1	HSTR4
26	31	100.0	103	1	HSTR4
27	31	100.0	103	2	S11312
28	31	100.0	103	2	D56618
29	31	100.0	103	2	S21367

30	31	100.0	103	2	B56580	histone H4 - midge
31	31	100.0	103	2	S10076	histone H4.2 - sil
32	31	100.0	103	2	A27859	histone H4.1 - sil
33	31	100.0	103	2	S09656	histone H4 - fruit
34	31	100.0	103	2	A25875	histone H4 - Tetra
35	31	100.0	103	2	S20677	histone H4 - starf
36	31	100.0	103	2	UH0507	histone H4.III and
37	31	100.0	103	2	S20666	histone H4 - starf
38	31	100.0	103	2	S20670	histone H4 - starf
39	31	100.0	103	2	S20668	histone H4 - starf
40	31	100.0	103	2	S01618	histone H4 - embryo
41	31	100.0	103	2	S49485	histone H4 - sea c
42	31	100.0	103	2	UH0688	histone H4 - sea b
43	31	100.0	103	2	S11940	histone H4.2 - Eme
44	31	100.0	103	2	S11939	histone H4.1 - Eme
45	31	100.0	103	2	S32769	histone H4 - tomal
46	31	100.0	103	2	S04240	histone H4 - Caeno
47	31	100.0	103	2	T27741	hypothetical prote
48	31	100.0	103	2	B56654	histone H4 - Tigri
49	31	100.0	103	2	S15433	histone H4 - Kenya
50	31	100.0	103	2	S15459	histone H4 - musco
51	31	100.0	103	2	S59586	histone H4 (clones
52	31	100.0	103	2	S00939	histone H4 - Volvo
53	31	100.0	103	2	S03427	histone H4 (clone
54	31	100.0	103	2	S03426	histone H4 - mouse
55	31	100.0	103	2	S07913	histone H4 - Neuro
56	31	100.0	103	2	B84688	histone H4 - Arabi
57	31	100.0	103	2	S06904	histone H4 - Arabi
58	31	100.0	104	2	S14184	histone H4 (clone
59	31	100.0	104	2	US0154	histone H4 - Oxytr
60	31	100.0	118	2	T29230	hypothetical prote
61	31	100.0	139	2	C84849	hypothetical prote
62	31	100.0	145	2	S14185	histone H4 (clone
63	31	100.0	155	2	T24840	hypothetical prote
64	31	100.0	198	2	H64359	hypothetical prote
65	31	100.0	211	2	B71809	hypothetical prote
66	31	100.0	211	2	B64710	hypothetical prote
67	31	100.0	211	2	S47347	outer membrane pro
68	31	100.0	212	2	A93370	hypothetical prote
69	31	100.0	215	2	S54203	keratin 6 - bovine
70	31	100.0	220	2	B64460	hypothetical prote
71	31	100.0	238	2	A81671	conserved hypotet
72	31	100.0	238	2	D71513	hypothetical prote
73	31	100.0	241	2	F90353	hypothetical prote
74	31	100.0	251	2	B72312	phosphoribosylamin
75	31	100.0	257	2	A36057	MHC class I histoc
76	31	100.0	279	1	D71067	hypothetical prote
77	31	100.0	287	2	B84226	fructose-bisphosph
78	31	100.0	316	2	H89995	sucrose operon rep
79	31	100.0	318	2	I39484	3-oxoacyl-lacyl-ca
80	31	100.0	332	2	D83745	hypothetical nucle
81	31	100.0	333	2	T37871	probable alcohol d
82	31	100.0	335	2	H87165	hypothetical prote
83	31	100.0	341	2	C75436	probable alcohol d
84	31	100.0	346	2	F70666	hypothetical prote
85	31	100.0	350	2	T18850	hypothetical prote
86	31	100.0	367	2	A84714	transcription regu
87	31	100.0	382	2	AC3118	actin-like protein
88	31	100.0	390	2	T38191	fric protein (AP19
89	31	100.0	402	2	D8169	multidrug resistan
90	31	100.0	418	2	B75087	conserved hypotet
91	31	100.0	419	2	C95091	conserved hypotet
92	31	100.0	419	2	G97958	conserved hypotet
93	31	100.0	454	2	A70079	conserved hypotet
94	31	100.0	458	2	D97799	NADH2 dehydrogenas
95	31	100.0	458	2	H71657	NADH2 dehydrogenas
96	31	100.0	459	2	E71443	probable DNA-bind
97	31	100.0	465	2	T27885	sperm membrane pro
98	31	100.0	467	2	I50476	keratin type I - g
99	31	100.0	469	2	A50166	conserved hypotet
100	31	100.0	497	2	A83884	L-arabinose isomer
101	31	100.0	500	2	A80274	L-arabinose isomer
102	31	100.0	513	2	F84371	tryptophanyl-tRNA

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# OM protein - protein search, using sw model

Run on: August 21, 2006, 23:30:51 ; Search time 299 Seconds

(without alignments)  
15,468 Million cell updates/sec

Title: US-10-766-527-1

Perfect score: 31

Sequence: 1 YGFGG 5

Scoring table: BLOSUM62

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	14	P70007 XENLA	P70007 xenopus lae
2	31	100.0	19	Q9N654 DROVI	Q9N654 drosophila
3	31	100.0	19	Q5BM22 RAT	Q5BM22 rattus norv
4	31	100.0	24	P91948 DROVI	P91948 drosophila
5	31	100.0	32	Q7M2K3 RABIT	Q7M2K3 coryctolagus
6	31	100.0	40	Q4YUL1 PLABE	Q4YUL1 plasmodium
7	31	100.0	45	Q27057 9TRYP	Q27057 trypanosoma
8	31	100.0	55	Q61667 MUSE	Q61667 mus musculu
9	31	100.0	58	Q7RG24 PLAYO	Q7RG24 plasmodium
10	31	100.0	58	Q38686 ALICE	Q38686 allium cepa
11	31	100.0	65	Q74P21 GEOSL	Q74P21 geobacter s
12	31	100.0	65	Q5WQD5 92Z22	Q5WQD5 uncultured
13	31	100.0	65	Q5WQD6 92Z22	Q5WQD6 uncultured
14	31	100.0	68	Q9U502 MANSE	Q9U502 manduca sex
15	31	100.0	78	Q3SF88 THIDA	Q3SF88 thiodacilla
16	31	100.0	81	Q418B9 GIBER	Q418B9 gibberella
17	31	100.0	81	Q38189 LACSS	Q38189 lactobacilli
18	31	100.0	85	Q25880 OVIS	Q25880 ovis aries
19	31	100.0	85	Q5S055 SHEEP	Q5S055 ovis aries
20	31	100.0	89	Q6R640 CAPHI	Q6R640 capra hircu
21	31	100.0	89	Q4PRB2 BRABR	Q4PRB2 brachydanto
22	31	100.0	92	MLP1 DROME	MLP1 drosophila
23	31	100.0	92	Q6B0K6 9CTUC	Q6B0K6 aptona ger
24	31	100.0	92	Q6X1G1 DROYA	Q6X1G1 drosophila
25	31	100.0	92	Q7Q080 ANOGA	Q7Q080 anopheles g
26	31	100.0	93	Q5BFE6 EMENT	Q5BFE6 aspergillus
27	31	100.0	94	Q5MGJ0 LONON	Q5MGJ0 lonoxia obl
28	31	100.0	94	Q6SA71 BOMMO	Q6SA71 bombyx mori
29	31	100.0	96	Q9412 EPISC	Q9412 epiblastema sc
30	31	100.0	96	Q3XV68 9PROT	Q3XV68 magnetococc
31	31	100.0	98	Q4T107 TESTING	Q4T107 tetradon n

32	31	100.0	102	1	H41 ASHCO	Q757k0 ashbya goes
33	31	100.0	102	1	H41 EMENT	Q23750 emericella
34	31	100.0	102	1	H41 PENFN	Q715m0 penicillium
35	31	100.0	102	1	H41 TETPY	P02310 tetrahymena
36	31	100.0	102	1	H41 WHBAT	P62785 triticum ae
37	31	100.0	102	1	H42 ASHCO	Q75ax1 ashbya goes
38	31	100.0	102	1	H42 EMENT	P23751 emericella
39	31	100.0	102	1	H42 PENFN	Q81q8 penicillium
40	31	100.0	102	1	H42 TETPY	P69152 tetrahymena
41	31	100.0	102	1	H42 TETTH	P69152 tetrahymena
42	31	100.0	102	1	H42 WHEAT	P62786 triticum ae
43	31	100.0	102	1	H43 MAIZE	Q41811 zea mays (m
44	31	100.0	102	1	H48 CHICK	P70081 gallus galli
45	31	100.0	102	1	H4 ACRAO	P84048 acrotopis
46	31	100.0	102	1	H4 ACROF	P35059 acropora fo
47	31	100.0	102	1	H4 APIME	P91849 apis mellif
48	31	100.0	102	1	H4 APICA	P59259 arabidopsis
49	31	100.0	102	1	H4 ARATH	Q8act8 arabidopsis
50	31	100.0	102	1	H4 ARXAD	Q81113 arxula aden
51	31	100.0	102	1	H4 ASCSU	Q27443 ascaris suu
52	31	100.0	102	1	H4 ASBAQ	P84047 asellus aqu
53	31	100.0	102	1	H4 ASPFU	Q71Kt3 aspergillus
54	31	100.0	102	1	H4 ASPOR	Q7cm7 aspergillus
55	31	100.0	102	1	H4 BOVIN	P62803 bos taurus
56	31	100.0	102	1	H4 CABEL	P62784 caenorhabdi
57	31	100.0	102	1	H4 CANMO	Q81q3 calina mos
58	31	100.0	102	1	H4 CANGA	Q81q3 candida gla
59	31	100.0	102	1	H4 CAPAN	Q71v09 capsicum an
60	31	100.0	102	1	H4 CHAVR	Q7qkd1 chaetopteru
61	31	100.0	102	1	H4 CHBMT	Q6pm15 chelidonium
62	31	100.0	102	1	H4 CHITK	P62801 gallus galli
63	31	100.0	102	1	H4 CHITP	P84046 chironomus
64	31	100.0	102	1	H4 CHLRE	P50566 chlamydomon
65	31	100.0	102	1	H4 DENKL	Q61af1 dendronept
66	31	100.0	102	1	H4 DIAPU	P91882 diadromus p
67	31	100.0	102	1	H4 DROBR	P84041 drosophila
68	31	100.0	102	1	H4 DROHY	P84042 drosophila
69	31	100.0	102	1	H4 DROMA	Q76f7 drosophila
70	31	100.0	102	1	H4 DROME	P84040 drosophila
71	31	100.0	102	1	H4 DROOR	Q76f1 drosophila
72	31	100.0	102	1	H4 DROSE	Q76f1 drosophila
73	31	100.0	102	1	H4 DROSI	P84043 drosophila
74	31	100.0	102	1	H4 DROVE	Q76f5 drosophila
75	31	100.0	102	1	H4 DROVA	P84044 drosophila
76	31	100.0	102	1	H4 EIMTE	Q87718 elmeria ten
77	31	100.0	102	1	H4 BUCGL	Q6z823 eucalyptus
78	31	100.0	102	1	H4 PIATR	Q61af3 flavetia tr
79	31	100.0	102	1	H4 HOLTU	P62776 holoturria
80	31	100.0	102	1	H4 HUMAN	P62805 homo sapien
81	31	100.0	102	1	H4 LOLTU	P62887 lolium temu
82	31	100.0	102	1	H4 LYCES	P35057 lycopersico
83	31	100.0	102	1	H4 LYTPI	P62782 lytechinus
84	31	100.0	102	1	H4 MAIZE	P62787 zea mays (m
85	31	100.0	102	1	H4 MORAP	Q9ndf5 mortierella
86	31	100.0	102	1	H4 MUSE	P62806 mus musculu
87	31	100.0	102	1	H4 MYRRU	P84045 myrmica rug
88	31	100.0	102	1	H4 MYTCA	Q6v73 mytilus cal
89	31	100.0	102	1	H4 MYTCH	Q6v74 mytilus cal
90	31	100.0	102	1	H4 MYTED	Q78c0 mytilus edu
91	31	100.0	102	1	H4 MYTGA	Q6v79 mytilus gal
92	31	100.0	102	1	H4 MYTTR	Q6v79 mytilus tro
93	31	100.0	102	1	H4 NEUCR	P04914 neurospora
94	31	100.0	102	1	H4 OLITU	P82888 olisthodisc
95	31	100.0	102	1	H4 ONCMY	P62797 oncorhynch
96	31	100.0	102	1	H4 ORENT	P62796 oreochromis
97	31	100.0	102	1	H4 PARLI	P62780 paracentroc
98	31	100.0	102	1	H4 PEA	P62788 pisum sativ
99	31	100.0	102	1	H4 PHYPO	P04915 physarum po
100	31	100.0	102	1	H4 PIG	P62802 sus scrofa
101	31	100.0	102	1	H4 PISBR	P62777 pisaster br
102	31	100.0	102	1	H4 PISOC	P62778 pisaster oc
103	31	100.0	102	1	H4 PIADI	P62795 platyneurus
104	31	100.0	102	1	H4 PSAMI	P62781 psammechinu

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OM protein - protein search, using sw model

Run on: February 17, 2005, 19:19:55 ; Search time 61 Seconds  
(without alignments)  
31.702 Million cell updates/sec

Title: **31**  
Perfect score: 31  
Sequence: 1 YGFGG 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 200 summaries

Database : A\_Geneseq\_1Dec04:\*

1: **Geneseqp2003as:\***  
2: Geneseqp2003bs:\*3: Geneseqp2003cs:\*4: Geneseqp2003ds:\*5: Geneseqp2003es:\*6: Geneseqp2003fs:\*7: Geneseqp2003gs:\*8: Geneseqp2003hs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	31	100.0	5	2	AAR76124 Osteogeni
2	31	100.0	5	2	ADC73222 Cyclic ps
3	31	100.0	5	2	ABP72525 Osteogeni
4	31	100.0	6	2	AAR62388 Osteoblas
5	31	100.0	6	2	AAR62954 Cyclic ps
6	31	100.0	6	2	ADC73230 Cyclic ps
7	31	100.0	6	2	ADC73233 Cyclic ps
8	31	100.0	6	2	ADC73229 Cyclic ps
9	31	100.0	6	2	ABP72528 Osteogeni
10	31	100.0	14	2	AAR06551 Osteogeni
11	31	100.0	14	2	AAR43890 Osteogeni
12	31	100.0	14	2	AAR43888 Osteogeni
13	31	100.0	14	2	AAR62952 Osteogeni
14	31	100.0	14	4	AAB92061 Growth fa
15	31	100.0	14	6	ABR63887 Osteogeni
16	31	100.0	14	6	ADA27392 Osteogeni
17	31	100.0	14	8	ADL35204 Human OGP
18	31	100.0	15	2	AAR43889 Osteogeni
19	31	100.0	17	2	AAR48440 Histogran
20	31	100.0	17	2	AAR48449 Histogran
21	31	100.0	17	2	AAR48442 Histogran
22	31	100.0	17	2	AAR48448 Histogran
23	31	100.0	17	2	AAR48444 Histogran
24	31	100.0	17	2	AAR48445 Histogran
25	31	100.0	17	2	AAR48450 Histogran

26	31	100.0	17	2	AAR48443 Histogran
27	31	100.0	17	2	AAR48447 Histogran
28	31	100.0	17	2	AAR48446 Histogran
29	31	100.0	17	2	AAR48441 Histogran
30	28	90.3	9	8	ADG94802 Human URM
31	28	90.3	9	8	ADL47148 Human-der
32	28	90.3	10	8	ADP87377 Human occ
33	28	90.3	10	8	ADG94749 Human URM
34	28	90.3	11	5	ABP75623 Anti-RANK
35	28	90.3	11	8	ADL47123 Permeabil
36	28	90.3	11	8	ADP87324 Human occ
37	27	87.1	12	4	AAB68835 Mycobacte
38	27	87.1	12	4	AAB68837 Escherich
39	27	87.1	12	4	AAB68822 Human FAS
40	27	87.1	12	4	AAB68823 Caenorhab
41	27	87.1	12	4	AAB68831 Barley KS
42	27	87.1	12	4	AAB68836 Escherich
43	27	87.1	12	4	AAB68821 Rat PAS P
44	27	87.1	12	4	AAB68833 Cuphea KS
45	27	87.1	12	4	AAB68832 Castor KS
46	27	87.1	12	4	AAB68834 Mycobacte
47	27	87.1	16	5	AAB22211 Tyrosinase
48	27	87.1	16	5	ABG32709 Mouse lna
49	27	87.1	16	5	ABG32710 Mouse lna
50	27	87.1	20	5	AAU90616 Insulin/i
51	27	87.1	20	5	AAU90937 Insulin/i
52	27	87.1	20	6	ADA04453 Insulin r
53	27	87.1	20	6	ADA04621 Insulin r
54	27	87.1	20	7	ADH95834 Insulin r
55	27	87.1	20	7	ADH95666 Insulin r
56	27	87.1	20	8	ADL68357 IGF-1R/IR
57	27	87.1	20	8	ADL68355 IGF-1R/IR
58	27	87.1	20	8	ADM8370 IR-bindin
59	27	87.1	20	8	ADM38202 Anti-IR m
60	25	80.6	4	2	ADC73221 Pseudopap
61	25	80.6	5	2	ADC73225 Pseudopap
62	25	80.6	6	2	ADC73227 Cyclic ps
63	25	80.6	6	2	ADC73228 Cyclic ps
64	25	80.6	6	2	ADC73231 Cyclic ps
65	25	80.6	6	2	AAB10740 ST3, conse
66	25	80.6	7	1	AAPI0567 Analgesic
67	25	80.6	8	2	AAR62416 Dipeteran
68	25	80.6	8	6	ABP72629 Calliphor
69	25	80.6	9	2	AAW72483 Dengue vi
70	25	80.6	9	2	AAW72488 Dengue vi
71	25	80.6	9	4	AAB68433 Human Bre
72	25	80.6	10	3	AAB24134 Plaemodiu
73	25	80.6	10	4	AAG84250 Arabidops
74	25	80.6	10	4	AAG84246 Arabidops
75	25	80.6	10	4	AAG84248 Arabidops
76	25	80.6	10	4	AAG87662 Saccharom
77	25	80.6	10	4	AAG87663 Saccharom
78	25	80.6	10	5	ABG95579 Human nov
79	25	80.6	10	6	ABO34473 Fragment
80	25	80.6	10	7	ADL23434 Novel hum
81	25	80.6	10	8	ADH74436 Human sec
82	25	80.6	11	2	AAR53983 Neurosept
83	25	80.6	12	2	AAR85460 Rust resi
84	25	80.6	12	4	AAH97122 Peptide m
85	25	80.6	13	2	AAR67982 Cockroach
86	25	80.6	13	2	AAB20393 Anti-Fix/
87	25	80.6	13	4	ABP91770 Allotocra
88	25	80.6	13	4	AAU03228 Fruit fly
89	25	80.6	13	6	ABP72614 Fruit plane
90	25	80.6	13	7	ADL14558 Drosophi
91	25	80.6	13	7	ADL83406 Drosophi
92	25	80.6	13	8	ADL91995 Allotocra
93	25	80.6	13	8	ADN03279 Exemplary
94	25	80.6	13	8	ADN03126 G-protein
95	25	80.6	14	2	ADR42114 Allostera
96	25	80.6	14	8	AAR62415 Dipeteran
97	25	80.6	14	6	ABP72628 Calliphor
98	25	80.6	15	2	AAW49179 Human leu





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OM protein - protein search, using SW model

Run on: February 17, 2005, 19:33:18 ; Search time 40 Seconds  
(without alignments)  
40.905 Million cell updates/sec

Title: US-10-766-527-1  
Perfect score: 31  
Sequence: 1 YGFGG 5

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1380268 segs, 327241040 residues

Total number of hits satisfying chosen parameters: 275641

Minimum DB seg length: 0  
Maximum DB seg length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 200 summaries

Database :

Pubmed Applications: 221  
1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
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17: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubppa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	5	14	US-10-255-679-4
2	31	100.0	5	14	US-10-255-679-6
3	31	100.0	5	14	US-10-255-679-7
4	31	100.0	5	14	US-10-255-679-8
5	31	100.0	5	14	US-10-255-679-9
6	31	100.0	5	14	US-10-255-679-10
7	31	100.0	5	14	US-10-255-679-10
8	31	100.0	5	14	US-10-255-679-10
9	31	100.0	5	14	US-10-255-679-10
10	31	100.0	5	14	US-10-255-679-10
11	31	100.0	5	14	US-10-255-679-10
12	31	100.0	5	14	US-10-255-679-10
13	31	100.0	5	14	US-10-255-679-10

14	31	100.0	5	14	US-10-255-679-51	Sequence 51, Appl
15	31	100.0	5	14	US-10-255-679-61	Sequence 61, Appl
16	31	100.0	5	16	US-10-766-527-1	Sequence 1, Appl
17	31	100.0	6	14	US-10-255-679-38	Sequence 38, Appl
18	31	100.0	6	14	US-10-255-679-39	Sequence 39, Appl
19	31	100.0	6	14	US-10-255-679-40	Sequence 40, Appl
20	31	100.0	6	14	US-10-255-679-41	Sequence 41, Appl
21	31	100.0	6	14	US-10-255-679-53	Sequence 53, Appl
22	31	100.0	6	14	US-10-255-679-59	Sequence 59, Appl
23	31	100.0	6	16	US-10-766-527-4	Sequence 4, Appl
24	31	100.0	14	14	US-10-255-679-1	Sequence 1, Appl
25	31	100.0	14	14	US-10-255-679-54	Sequence 54, Appl
26	31	100.0	14	14	US-10-255-679-55	Sequence 55, Appl
27	31	100.0	14	14	US-10-088-905-3	Sequence 3, Appl
28	31	100.0	15	15	US-10-437-435-13	Sequence 13, Appl
29	31	90.3	9	15	US-10-462-953-781	Sequence 781, Appl
30	31	90.3	9	15	US-10-601-953-859	Sequence 859, Appl
31	31	90.3	9	16	US-10-322-666-782	Sequence 782, Appl
32	31	90.3	11	15	US-10-344-779-10	Sequence 10, Appl
33	31	90.3	11	15	US-10-462-452-728	Sequence 728, Appl
34	31	90.3	11	15	US-10-601-953-833	Sequence 833, Appl
35	31	90.3	11	16	US-10-322-666-729	Sequence 729, Appl
36	31	90.3	11	16	US-10-738-809-10	Sequence 10, Appl
37	31	87.1	5	14	US-10-255-679-24	Sequence 24, Appl
38	31	87.1	5	14	US-10-255-679-25	Sequence 25, Appl
39	31	87.1	6	14	US-10-255-679-26	Sequence 26, Appl
40	31	87.1	16	9	US-09-473-872-1	Sequence 1, Appl
41	31	87.1	16	9	US-09-473-872-5	Sequence 5, Appl
42	31	87.1	16	9	US-09-962-628B-36	Sequence 36, Appl
43	31	87.1	20	10	US-09-962-628B-1084	Sequence 1084, Appl
44	31	87.1	20	10	US-09-962-628B-1252	Sequence 1252, Appl
45	31	87.1	20	15	US-10-253-471-1084	Sequence 1084, Appl
46	31	87.1	20	15	US-10-253-471-1252	Sequence 1252, Appl
47	31	87.1	20	15	US-10-253-493-1084	Sequence 1084, Appl
48	31	87.1	20	15	US-10-253-493-1252	Sequence 1252, Appl
49	31	87.1	4	14	US-10-255-679-11	Sequence 11, Appl
50	31	80.6	4	14	US-10-255-679-12	Sequence 12, Appl
51	31	80.6	4	14	US-10-255-679-13	Sequence 13, Appl
52	31	80.6	4	14	US-10-255-679-36	Sequence 36, Appl
53	31	80.6	5	14	US-10-255-679-18	Sequence 18, Appl
54	31	80.6	5	14	US-10-255-679-22	Sequence 22, Appl
55	31	80.6	5	14	US-10-255-679-23	Sequence 23, Appl
56	31	80.6	5	14	US-10-255-679-28	Sequence 28, Appl
57	31	80.6	5	14	US-10-255-679-29	Sequence 29, Appl
58	31	80.6	5	14	US-10-255-679-32	Sequence 32, Appl
59	31	80.6	5	14	US-10-255-679-34	Sequence 34, Appl
60	31	80.6	5	14	US-10-255-679-43	Sequence 43, Appl
61	31	80.6	6	14	US-10-255-679-44	Sequence 44, Appl
62	31	80.6	6	14	US-10-255-679-45	Sequence 45, Appl
63	31	80.6	6	14	US-10-255-679-46	Sequence 46, Appl
64	31	80.6	9	10	US-09-988-993-280	Sequence 280, Appl
65	31	80.6	10	10	US-09-809-191-719	Sequence 719, Appl
66	31	80.6	10	10	US-09-572-270A-886	Sequence 886, Appl
67	31	80.6	10	10	US-09-572-270A-888	Sequence 888, Appl
68	31	80.6	10	10	US-09-572-270A-890	Sequence 890, Appl
69	31	80.6	10	10	US-09-882-171-719	Sequence 719, Appl
70	31	80.6	10	15	US-10-164-661-719	Sequence 719, Appl
71	31	80.6	13	14	US-10-283-423-36	Sequence 36, Appl
72	31	80.6	13	14	US-10-283-423-36	Sequence 36, Appl
73	31	80.6	13	14	US-10-283-423-36	Sequence 36, Appl
74	31	80.6	13	15	US-10-360-101-75	Sequence 75, Appl
75	31	80.6	13	15	US-10-360-101-75	Sequence 75, Appl
76	31	80.6	13	16	US-10-736-048-36	Sequence 36, Appl
77	31	80.6	17	9	US-09-944-849-9	Sequence 9, Appl
78	31	80.6	17	9	US-09-944-849-11	Sequence 11, Appl
79	31	80.6	17	9	US-09-944-849-12	Sequence 12, Appl
80	31	80.6	17	9	US-09-944-849-12	Sequence 12, Appl
81	31	80.6	17	9	US-09-944-849-12	Sequence 12, Appl
82	31	80.6	17	9	US-09-944-849-12	Sequence 12, Appl
83	31	80.6	17	9	US-09-944-849-12	Sequence 12, Appl
84	31	80.6	17	9	US-09-944-849-12	Sequence 12, Appl
85	31	80.6	17	9	US-09-944-849-12	Sequence 12, Appl
86	31	80.6	17	9	US-09-944-849-12	Sequence 12, Appl

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OM protein - protein search, using sw model

Run on: February 17, 2005, 19:27:01 ; Search time 11.25 Seconds

(without alignments)  
42.763 Million cell updates/sec

Title: ~~US-10-766-527-1~~

Perfect score: 3.1

Sequence: 1 YGFGG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	14	2	I51432
2	31	100.0	18	2	C30309
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4	24	77.4	14	2	A17150
5	23	74.2	13	2	A33933
6	22	71.0	10	2	C45474
7	22	71.0	17	2	S33609
8	22	71.0	20	2	PH1341
9	21	67.7	10	2	F60527
10	21	67.7	14	2	E33098
11	21	67.7	15	2	PC4269
12	21	67.7	20	2	A61525
13	20	64.5	18	2	S20332
14	19	61.3	7	1	A61324
15	19	61.3	7	2	S36662
16	19	61.3	8	2	D47393
17	19	61.3	10	2	A60589
18	19	61.3	13	2	S48210
19	19	61.3	15	2	B56978
20	19	61.3	16	2	T44936
21	19	61.3	17	2	S09085
22	19	61.3	20	2	P80087
23	19	58.1	4	2	A53284
24	18	58.1	7	2	H33098
25	18	58.1	7	2	PT0725
26	18	58.1	8	2	PT0725
27	18	58.1	8	2	PC4373
28	18	58.1	8	2	PC4373
29	18	58.1	9	2	D24180

30	18	58.1	9	2	F28854	fibriopeptide B -
31	18	58.1	9	2	PT0225	Ig heavy chain CDR
32	18	58.1	9	2	S10784	enamelin I - bovin
33	18	58.1	9	2	PC7074	translation elonga
34	18	58.1	10	2	PT0632	T-cell receptor be
35	18	58.1	10	2	PT0664	T-cell receptor be
36	18	58.1	10	2	S06964	hypothetical prote
37	18	58.1	10	2	B60589	sperm-activating p
38	18	58.1	11	2	A44755	20alpha-hydroxyste
39	18	58.1	12	2	A49261	coagulation factor
40	18	58.1	12	2	A58375	microcin B17 - Bsc
41	18	58.1	13	2	PT0263	Ig heavy chain CRD
42	18	58.1	13	2	B20907	Ig kappa-1 chain J
43	18	58.1	13	2	B26406	Ig kappa chain J r
44	18	58.1	13	2	S22761	Ig lambda-2 chain
45	18	58.1	13	2	A47630	Ig kappa chain J r
46	18	58.1	13	2	PS0277	glyceroldehyde-3-p
47	18	58.1	14	2	PH0747	T-cell receptor be
48	18	58.1	15	2	A26228	spot 42 protein -
49	18	58.1	15	2	JT0610	leukocyte chemoat
50	18	58.1	16	2	A12729	glutamate dehydrog
51	18	58.1	16	2	S11805	heat shock protein
52	18	58.1	16	2	A29520	amino-acid racemas
53	18	58.1	18	2	B32473	histidine-rich pro
54	18	58.1	18	2	PH1792	T cell receptor al
55	18	58.1	18	2	S47196	T-cell receptor J r
56	18	58.1	18	2	S40502	20-alpha-hydroxyst
57	18	58.1	19	2	A28814	Ig kappa chain V r
58	18	58.1	19	2	A39504	octamer-binding pr
59	18	58.1	19	2	S68393	H+-transporting tw
60	18	58.1	19	2	S74087	antibacterial prot
61	18	58.1	19	2	B48138	d(TTACGCG)n-binding
62	18	58.1	20	2	S17501	glutaminase - Alca
63	18	58.1	20	2	PA0115	protein QR200034 -
64	17	54.8	8	2	PH1618	Ig H chain V-D-U r
65	17	54.8	12	2	S26548	T-cell receptor be
66	17	54.8	12	2	S26544	T-cell receptor be
67	17	54.8	12	2	S26547	T-cell receptor be
68	17	54.8	12	2	S26546	T-cell receptor be
69	17	54.8	12	2	S26541	T-cell receptor be
70	17	54.8	12	2	PH1458	T-cell receptor be
71	17	54.8	12	2	PH1462	T-cell receptor be
72	17	54.8	12	2	PH1461	T-cell receptor be
73	17	54.8	12	2	PH1457	T-cell receptor be
74	17	54.8	12	2	PH1459	T-cell receptor be
75	17	54.8	13	2	C47630	Ig kappa chain J r
76	17	54.8	14	2	S23639	Ig kappa chain J s
77	17	54.8	14	2	A32654	fibriopeptide A -
78	17	54.8	15	2	H56978	collagen alpha 1(X
79	17	54.8	16	1	MTDPBS	melanotropin beta
80	17	54.8	16	2	S57517	T cell receptor be
81	17	54.8	16	2	C49048	T-cell receptor be
82	17	54.8	16	2	PH1473	T-cell receptor be
83	17	54.8	16	2	S28433	major outer membra
84	17	54.8	17	2	H49048	T-cell receptor be
85	17	54.8	17	2	I49048	T-cell receptor be
86	17	54.8	17	2	PH1367	Ig heavy chain DJ
87	17	54.8	17	2	I67324	CD33 antigen homol
88	17	54.8	17	2	PH1323	Ig heavy chain DJ
89	17	54.8	18	2	B49048	T-cell receptor be
90	17	54.8	18	2	P00072	T-cell receptor be
91	17	54.8	18	2	B48839	T-cell receptor be
92	17	54.8	19	2	A44379	alpha-conotoxin SI
93	17	54.8	19	2	G49048	T-cell receptor be
94	17	54.8	19	2	PT0332	Ig heavy chain CRD
95	17	54.8	19	2	E49048	T-cell receptor be
96	17	54.8	20	2	PS0332	phospholipase A2 (
97	17	54.8	20	2	F49048	T-cell receptor be
98	17	54.8	20	2	A49048	T-cell receptor be
99	17	54.8	20	2	B61577	17.6k serine prote
100	17	54.8	20	2	A54042	mannose-6-phosphat
101	17	54.8	20	2	A60801	actosome stabilizi
102	16	51.6	5	2	C53284	T-cell receptor be

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 17, 2005, 19:26:05 ; Search time 77.5 Seconds  
(without alignments)  
33.037 Million cell updates/sec

Title: US-10-766-527-1  
Perfect score: 31  
Sequence: 1 YGFCG 5

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database :

1: ~~uniprot\_sprot~~:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	31	100.0	14 2 P70007	P70007 xenopus lae
2	31	100.0	19 2 Q9N654	Q9N654 drosophila
3	25	80.6	16 1 AL11_CALVO	P41839 calliphora
4	24	77.4	19 2 Q85671	Q85671 recivitus ty
5	24	77.4	20 1 K0RC_METTM	P80906 mechanobact
6	24	77.4	20 2 Q85670	Q85670 recivitus ty
7	23	74.2	11 2 Q70Y64	Q70Y64 plectranthu
8	23	74.2	17 2 Q6EX59	Q6EX59 thymus serp
9	23	74.2	17 2 Q9QV41	Q9QV41 mus sp. . g
10	22	71.0	11 2 Q9TWM2	Q9TWM2 aplysia cal
11	22	71.0	17 2 Q9S857	Q9S857 zea.mays (m
12	22	71.0	19 2 Q6LDN4	Q6LDN4 rhodobacter
13	21	67.7	10 1 CU30_LOCM1	P11735 locustra.mlg
14	21	67.7	10 2 Q7M3T9	Q7M3T9 tirpneutes
15	21	67.7	14 2 Q86922	Q86922 human cytom
16	21	67.7	20 2 Q9TRCO	Q9TRCO bos taurus
17	20	64.5	13 2 Q9UDR0	Q9UDR0 homo sapien
18	20	64.5	17 2 Q9TR22	Q9TR22 bos taurus
19	20	64.5	18 2 Q7M1G0	Q7M1G0 triticum ae
20	19	61.3	5 1 AL14_CARMA	P81817 carcins ma
21	19	61.3	7 1 AL12_CARMA	P81805 carcins ma
22	19	61.3	7 1 AL13_CARMA	P81806 carcins ma
23	19	61.3	7 1 AL14_CARMA	P81807 carcins ma
24	19	61.3	7 1 AL15_CARMA	P81808 carcins ma
25	19	61.3	8 1 AL12_CARMA	P81815 carcins ma
26	19	61.3	8 1 AL15_CARMA	P81816 carcins ma
27	19	61.3	8 1 AL17_CARMA	P81820 carcins ma
28	19	61.3	8 1 AL18_CARMA	P81821 carcins ma
29	19	61.3	8 1 AL11_CYDPO	P82152 cydia pomon
30	19	61.3	8 1 AL13_CYDPO	P82154 cydia pomon
31	19	61.3	8 1 AL14_CALVO	P41840 calliphora
32	19	61.3	8 1 AL14_CYDPO	P82155 cydia pomon
33	19	61.3	8 1 AL16_CYDPO	P82157 cydia pomon
34	19	61.3	8 1 AL17_CARMA	P81809 carcins ma
35	19	61.3	8 1 AL18_CARMA	P81811 carcins ma
36	19	61.3	8 1 AL19_CARMA	P81812 carcins ma
37	19	61.3	9 1 AL10_CARMA	P81813 carcins ma
38	19	61.3	9 1 AL11_CARMA	P81814 carcins ma
39	19	61.3	9 2 P83529	P83529 lactobacilli
40	19	61.3	10 1 AL19_CARMA	P81822 carcins ma
41	19	61.3	10 2 Q7M4E7	Q7M4E7 heterocentr
42	19	61.3	13 1 ADPB_TENNO	P83109 tenedrio mo
43	19	61.3	13 2 Q9UJ73	Q9UJ73 homo sapien
44	19	61.3	13 2 Q9TQ05	Q9TQ05 bos taurus
45	19	61.3	16 2 Q94554	Q94554 schizosacch
46	19	61.3	16 2 Q96T80	Q96T80 homo sapien
47	19	61.3	16 2 Q9TRM2	Q9TRM2 bos taurus
48	19	61.3	16 2 Q99374	Q99374 staphylococ
49	19	61.3	18 1 AL13_CARMA	P81816 carcins ma
50	19	61.3	18 1 AL12_CYDPO	P82153 cydia pomon
51	18	58.1	18 1 OCCP1_OCTM1	P58648 octopus min
52	18	58.1	7 1 AL17_CYDPO	P82158 cydia pomon
53	18	58.1	8 1 AL15_CALVO	P41841 calliphora
54	18	58.1	8 1 AL15_CYDPO	P82156 cydia pomon
55	18	58.1	8 2 Q7M032	Q7M032 rattus norv
56	18	58.1	9 1 F1BB_ERYPA	P19346 erythrocebu
57	18	58.1	9 1 F1BB_THREE	P19342 theopithec
58	18	58.1	9 2 Q7M2M7	Q7M2M7 bos taurus
59	18	58.1	10 2 Q7M4B9	Q7M4B9 heterocentr
60	18	58.1	10 2 Q52837	Q52837 rhizobium l
61	18	58.1	11 2 Q7M1A0	Q7M1A0 eubacterium
62	18	58.1	12 2 Q7L226	Q7L226 agkistrodon
63	18	58.1	13 1 ORCK_ORCLI	P73086 orconectes
64	18	58.1	13 2 Q9U572	Q9U572 trypanosoma
65	18	58.1	14 1 F1BB_MANIE	P14474 mandrillus
66	18	58.1	14 2 Q8J1G0	Q8J1G0 asbaya goss
67	18	58.1	14 2 Q9TR07	Q9TR07 bos taurus
68	18	58.1	14 2 Q85718	Q85718 recivitus ty
69	18	58.1	14 2 Q6SEH0	Q6SEH0 umbra limi
70	18	58.1	15 1 TRPA_LEUMA	P81753 leucophaea
71	18	58.1	15 2 Q9TWF3	Q9TWF3 dictyosteli
72	18	58.1	15 2 Q9TWS0	Q9TWS0 pyura stolo
73	18	58.1	15 2 Q7M2Q2	Q7M2Q2 ovis aries
74	18	58.1	15 2 Q9S808	Q9S808 ricinus com
75	18	58.1	15 2 P82468	P82468 pseudomonas
76	18	58.1	15 2 Q46963	Q46963 escherichia
77	18	58.1	15 2 Q7CPD2	Q7CPD2 salmoneila
78	18	58.1	16 1 ALRX_PSEBU	P17916 pseudomonas
79	18	58.1	16 1 DHE2_THUTH	P20016 thunnus thy
80	18	58.1	16 2 Q9R5S9	Q9R5S9 treponema d
81	18	58.1	17 1 PNOG_PIG	P55791 sus scrofa
82	18	58.1	17 2 Q9HBD8	Q9HBD8 homo sapien
83	18	58.1	17 2 Q9Y3F6	Q9Y3F6 homo sapien
84	18	58.1	17 2 Q9TQ25	Q9TQ25 macaca faec
85	18	58.1	17 2 Q8GJN9	Q8GJN9 lactococcus
86	18	58.1	17 2 Q9QVH8	Q9QVH8 mus sp. . ryp
87	18	58.1	17 2 Q64973	Q64973 alfalfa mos
88	18	58.1	17 2 Q64974	Q64974 alfalfa mos
89	18	58.1	18 1 AH22_TETPY	P35430 tetraymena
90	18	58.1	18 1 G3P_NAEFO	P83630 naegleria f
91	18	58.1	18 2 Q7M3X9	Q7M3X9 fasciola he
92	18	58.1	18 2 Q6A3S7	Q6A3S7 archangiolo
93	18	58.1	18 2 Q6A417	Q6A417 archangiolo
94	18	58.1	18 2 Q6A4A1	Q6A4A1 archangiolo
95	18	58.1	18 2 Q6A4B7	Q6A4B7 archangiolo
96	18	58.1	18 2 Q6A4B9	Q6A4B9 archangiolo
97	18	58.1	18 2 Q6A4C1	Q6A4C1 archangiolo
98	18	58.1	19 1 AB27_CYPCA	P81925 cyprinus ca
99	18	58.1	19 1 RS19_SPTCI	RS19_SPTCI
100	18	58.1	19 2 Q9UCB9	Q9UCB9 spirloplasma
101	18	58.1	19 2 Q9N1W2	Q9N1W2 equus cabal
102	18	58.1	19 2 Q9TRR6	Q9TRR6 oryctolagus
103	18	58.1	19 2 Q05601	Q05601 pseudomonas
104	18	58.1	19 2 Q64GH8	Q64GH8 legionella